IN THE CLAIMS:

Applicant, pursuant to 37 C.F.R. § 1.121, submits the following amendments to the claims:

1. (Currently amended) A method for detecting methylated nucleic acids comprising ~~the steps of~~:

~~(i)~~ contacting a nucleic acid sample suspected of containing methylated nucleotides with an oligonucleotide probe under suitable conditions for nucleic acid hybridization, said oligonucleotide probe ~~characterized in that,~~

~~(a) it comprises~~ comprising a first stem labeled with a fluorophore moiety, a loop sequence having a region of nucleotides complementary to at least a region of the nucleic acid ~~sample, which region of the nucleic acid sample~~ that is susceptible to methylation, and a second stem labeled with a quencher moiety that is capable of quenching the fluorophore moiety when in sufficient spatial proximity to the fluorophore moiety,[[;]] and wherein

~~(b)~~ the nucleotides forming the first stem are capable of moving into spatial proximity with the nucleotides forming the second stem when the probe is dissociated from the nucleic acid sample;

~~(ii)~~ altering the hybridization conditions such that the oligonucleotide probe dissociates from unmethylated nucleic acids but remains hybridized to methylated nucleic acids; and

~~(iii)~~ measuring the change in fluorescence,[[;]]

wherein an increase in fluorescence indicates methylated nucleotides in said nucleic acid sample.

2. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein upon probe dissociation ~~the oligonucleotide probe dissociates~~ from the target nucleic acid ~~sample according to step (ii)~~ the first and second stem hybridize together causing quenching of the fluorophore moiety.

3. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein the loop sequence contains at least 10 nucleotides.

4. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein the loop sequence contains at least 35 nucleotides.

5. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein the loop sequence contains at least 25 nucleotides.

6. (Currently amended) The [[A]] method of ~~according to~~ claim 1,1 wherein the loop sequence contains from about 15 to about 20 nucleotides.

7. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein when the loop sequence is complementary to a portion of a nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

8. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein when the loop sequence is complementary to a portion of a Myf-3 nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

9. (Currently amended) The [[A]] method of ~~according to~~ claim 8, wherein the loop sequence is complementary to at least one of the sequences selected form the group consisting of SEQ ID NOS:1-3 and methylated CpG-containng variants thereof~~:~~

~~(i) 5' GCG GCG ACT CCG ACG CGT CCA GCC CGC GCT CC 3' (SEQ ID NO: 1);~~

~~(ii) 5' TTA TAC CGC AGG CGG GCG AGC CGC GGG CGC TCG CT 3' (SEQ ID NO: 2); and~~

~~(iii) 5' CCG AGA GCC CTG CGG GGC CCG CCC TCC TGC TGG CG 3' (SEQ ID NO: 3)~~.

10. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein when the loop sequence is complementary to a portion of a glutathionine-S-transferase-II (pi) nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous

state.

11. (Currently amended) The [[A]] method of ~~according to~~ claim 10, wherein the loop sequence is complementary to at least one of the sequences selected from the group consisting of SEQ ID NOS:4-5 and methylated CpG-containng variants thereof~~:~~

~~(i) 5' CTC CAG CGA AGG CCT CGC GGC CTC CGA GCC TTA TAA G 3' (SEQ ID NO: 4); AND~~

~~(ii) 5' GGG GAC GCG GGC CGC GCG TAC TCA CTG GTG GCG A 3' (SEQ ID NO: 5)~~.

12. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein when the loop sequence is complementary to a portion of a calcitonin nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

13. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein the method is used to detect abnormally methylated gene sequences in prostate cancer tissues.

14. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein altering the hybridization conditions ~~that is altered during the hybridization reaction is the~~ comprises altering the temperature of the hybridization reaction.

15. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein the stem sequences do not hybridise to the target gene and are of a sufficiently short length to avoid non-specific binding between the stem and any other nucleic acid sequence in the reaction mixture.

16. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein the stem sequences are at least ~~about~~ 4 to 8 nucleotides in length.

17. (Currently amended) The [[A]] method of ~~according to~~ claim 1, wherein at least ~~a cytosine in at least~~ one of the stem sequences contains a methylated cytosine residue.

18. (Canceled).